In the Specification:

Please replace the paragraph beginning at page 2, line 32, with the following:

A1

--The present invention provides methods of modulating mycorhizal infection in a plants. The method comprise introducing into the plant an expression cassette containing a plant promoter operably linked to a heterologous LNP polynucleotide or complement thereof, wherein the LNP polynucleotide encodes an LNP polypeptide at least about 70% identical to SEQ ID NO:2, SEQ ID NO:4, or SEQ ID NO:10. The heterologous LNP polynucleotide can be SEQ ID NO:1. SEQ ID NO:3, or SEQ ID NO:8.--

Please replace the paragraph beginning at page 5, line 18, with the following:

A2

--An "LNP polynucleotide" is a nucleic acid sequence comprising (or consisting of) a coding region of about 100 to about 2000 nucleotides, sometimes from about 1400 to about 1500 nucleotides, which specifically hybridizes, to the *Dolichos biflorus* polynucleotide (SEQ ID NO:1), or to the *Lotus japonicus* polynucleotide (SEQ ID NO:8), or to the *Medicago sativa* polynucleotide (SEQ ID NO:3), or which encodes an LNP polypeptide. The isolation and characterization of the *Lotus* and *Medicago* genes are described in the PCT application WO 98/16261.--

Please replace the paragraph beginning at page 5, line 25, with the following:

A3

--An LNP polypeptide of the present invention comprises at least 50 amino acids, more preferably at least 100 amino acids, still more preferably at least 200 amino acids and most preferably up to about 500 amino acids from SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:10 SEQ ID NO:6, and conservatively modified varients

A3

thereof. The LNP polypeptides of the present invention also include proteins which have substantial identity to an LNP protein of at least 10 to 500 amino acids selected from SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:10 SEQ ID NO:6 and conservatively modified variants thereof.--

Please replace the paragraph beginning at page 11, line 9, with the following:

A4

--In the present invention, genomic DNA or cDNA comprising LNP nucleic acids of the invention can be identified in standard Southern blots under stringent conditions using the nucleic acid sequences disclosed here. For the purposes of this disclosure, suitable stringent conditions for such hybridizations are those which include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and at least one wash in 0.2X SSC at a temperature of at least about 50°C, usually about 55°C to about 60°C, for 20 minutes, or equivalent conditions. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.--

Please replace the paragraph beginning at page 13, line 9, with the following:

A5

--Appropriate primers and probes for identifying LNP genes from Dolichos biflorus or transgenic plant tissues are generated from comparisons of the sequences provided herein. For a general overview of PCR see PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS, (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Appropriate degenerate primers for this invention include, for instance: a 5' PCR primer [5'-TA(T/C)GCNGTNAT(T/C)TT(T/C)GATGC-3'] (SEQ ID NO:13) and a 3' PCR primer [5'-AT(A/G)TT(A/G)TA(T/A/G)AT(G/A)CCNGG-3'] (SEQ ID NO:14) where N denotes all nucleotides. The amplification conditions are typically as follows. Reaction components: 10 mM Tris-HCl, pH 8.3, 50 mM potassium chloride, 1.5 mM magnesium

chloride, 0.001% gelatin, 200 μM dATP, 200 μM dCTP, 200 μM dGTP, 200 μM dTTP, 0.4 μM primers, and 100 units per mL Taq polymerase. Program: 96°C for 3 min., 30 cycles of 96°C for 45 sec., 50°C for 60 sec., 72°C for 60 sec, followed by 72°C for 5 min.--

Please replace the paragraph beginning at page 13, line 25, with the following:

--A preferred method is RACE (Frohman, et. al., *Proc. Nat'l. Acad. Sci. USA* 85:8998 (1988)). Briefly, this technique involves using PCR to amplify a DNA sequence using a random 5' primer and a defined 3' primer, e.g., (5' RACE) or a random 3' primer and a defined 5' primer, e.g., (3' RACE). The amplified sequence is then subcloned into a vector where it is then sequenced using standard techniques. Kits to perform RACE are commercially available (e.g. 5' RACE System, GIBCO BRL, Grand Island, New York, USA). In this manner, the entire LNP coding sequence of about 1600 bp can be obtained (SEQ ID NO:1). The invention also provides genomic sequence of the LNP (SEQ ID NO:3).--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 13, at the end of the application.